1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/469,200C

DATE: 09/05/2002
TIME: 08:43:23

Errors on p. 3

Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\09052002\I469200C.raw

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 3 <110> APPLICANT: Weigel, Paul H.
 4       DeAngelis, Paul
 5       Kumari, Kshama
 7 <120> TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof
 9 <130> FILE REFERENCE: 3554.011
11 <140> CURRENT APPLICATION NUMBER: US 09/469,200C
12 <141> CURRENT FILING DATE: 1999-12-21
14 <150> PRIOR APPLICATION NUMBER: US 09/178,851
15 <151> PRIOR FILING DATE: 1998-10-26
17 <150> PRIOR APPLICATION NUMBER: US 60/064,435
18 <151> PRIOR FILING DATE: 1997-10-31
20 <160> NUMBER OF SEQ ID NOS: 10
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1254
26 <212> TYPE: DNA
27 <213> ORGANISM: Streptococcus equisimilis
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30 atgagaacat taaaaaacct cataactgtt gtggccttta gtattttttg ggtactgttg     60
32 atttacgtca atgtttatct ctttggtgct aaaggaagct tgtcaattta tggctttttg    120
34 ctgatagctt acctattagt caaaatgtcc ttatcctttt tttacaagcc atttaaggga    180
36 agggctgggc aatataaggt tgcagccatt attccctctt ataacgaaga tgctgagtca    240
38 ttgctagaga ccttaaaaag tgttcagcag caaacctatc ccctagcaga aatttatgtt    300
40 gttgacgatg gaagtgctga tgagacaggt attaagcgca ttgaagacta tgtgcgtgac    360
42 actggtgacc tatcaagcaa tgtcattgtt catcggtcag agaaaaatca aggaaagcgt    420
44 catgcacagg cctgggcctt tgaaagatca gacgctgatg tctttttgac cgttgactca    480
46 gatacttata tctaccctga tgctttagag gagttgttaa aaacctttaa tgacccaact    540
48 gttttttgctg cgacgggtca ccttaatgtc agaaatagac aaaccaatct cttaacacgc    600
50 ttgacagata ttcgctatga taatgctttt ggcgttgaac gagctgccca atccgttaca    660
52 ggtaatatcc ttgtttgctc aggtccgctt agcgtttaca dacgcgaggt ggttgttcct    720
54 aacatagata gatacatcaa ccagaccttc ctgggtattc ctgtaagtat tggtgatgac    780
56 aggtgcttga ccaactatgc aactgattta ggaaagactg tttatcaatc cactgctaaa    840
58 tgtattacag atgttcctga caagatgtct acttacttga agcagcaaaa ccgctggaac    900
60 aagtccttct ttagagagtc cattatttct gttaagaaaa tcatgaacaa tccttttgta    960
62 gccctatgga ccatacttga ggtgtctatg tttatgatgc ttgtttattc tgtggtggat   1020
64 ttctttgtag gcaatgtcag agaatttgat tggctcaggg ttttagcctt tctggtgatt   1080
66 atcttcattg ttgccctgtg tcggaacatt cattacatgc ttaagcaccc gctgtccttc   1140
68 ttgttatctc cgtttttatgg ggtgctgcat ttgtttgtcc tacagccctt gaaattatat   1200
70 tctctttttta ctattagaaa tgctgactgg ggaacacgta aaaaattatt ataa         1254
73 <210> SEQ ID NO: 2
74 <211> LENGTH: 417
75 <212> TYPE: PRT
76 <213> ORGANISM: Streptococcus Equisimilis
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RAW SEQUENCE LISTING   DATE: 09/05/2002
PATENT APPLICATION: US/09/469,200C   TIME: 08:43:23

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81 1               5                  10                  15
84 Trp Val Leu Leu Ile Tyr Val Asn Val Tyr Leu Phe Gly Ala Lys Gly
85              20                  25                  30
88 Ser Leu Ser Ile Tyr Gly Phe Leu Leu Ile Ala Tyr Leu Leu Val Lys
89          35                  40                  45
92 Met Ser Leu Ser Phe Phe Tyr Lys Pro Phe Lys Gly Arg Ala Gly Gln
93      50                  55                  60
96 Tyr Lys Val Ala Ala Ile Ile Pro Ser Tyr Asn Glu Asp Ala Glu Ser
97 65                  70                  75                  80
100 Leu Leu Glu Thr Leu Lys Ser Val Gln Gln Gln Thr Tyr Pro Leu Ala
101              85                  90                  95
104 Glu Ile Tyr Val Val Asp Asp Gly Ser Ala Asp Glu Thr Gly Ile Lys
105              100                 105                 110
108 Arg Ile Glu Asp Tyr Val Arg Asp Thr Gly Asp Leu Ser Ser Asn Val
109              115                 120                 125
112 Ile Val His Arg Ser Glu Lys Asn Gln Gly Lys Arg His Ala Gln Ala
113      130                 135                 140
116 Trp Ala Phe Glu Arg Ser Asp Ala Asp Val Phe Leu Thr Val Asp Ser
117 145                 150                 155                 160
120 Asp Thr Tyr Ile Tyr Pro Asp Ala Leu Glu Glu Leu Leu Lys Thr Phe
121              165                 170                 175
124 Asn Asp Pro Thr Val Phe Ala Ala Thr Gly His Leu Asn Val Arg Asn
125              180                 185                 190
128 Arg Gln Thr Asn Leu Leu Thr Arg Leu Thr Asp Ile Arg Tyr Asp Asn
129          195                 200                 205
132 Ala Phe Gly Val Glu Arg Ala Ala Gln Ser Val Thr Gly Asn Ile Leu
133      210                 215                 220
136 Val Cys Ser Gly Pro Leu Ser Val Tyr Arg Arg Glu Val Val Val Pro
137 225                 230                 235                 240
140 Asn Ile Asp Arg Tyr Ile Asn Gln Thr Phe Leu Gly Ile Pro Val Ser
141              245                 250                 255
144 Ile Gly Asp Asp Arg Cys Leu Thr Asn Tyr Ala Thr Asp Leu Gly Lys
145              260                 265                 270
148 Thr Val Tyr Gln Ser Thr Ala Lys Cys Ile Thr Asp Val Pro Asp Lys
149          275                 280                 285
152 Met Ser Thr Tyr Leu Lys Gln Gln Asn Arg Trp Asn Lys Ser Phe Phe
153      290                 295                 300
156 Arg Glu Ser Ile Ile Ser Val Lys Lys Ile Met Asn Asn Pro Phe Val
157 305                 310                 315                 320
160 Ala Leu Trp Thr Ile Leu Glu Val Ser Met Phe Met Met Leu Val Tyr
161              325                 330                 335
164 Ser Val Val Asp Phe Phe Val Gly Asn Val Arg Glu Phe Asp Trp Leu
165              340                 345                 350
168 Arg Val Leu Ala Phe Leu Val Ile Ile Phe Ile Val Ala Leu Cys Arg
169          355                 360                 365
172 Asn Ile His Tyr Met Leu Lys His Pro Leu Ser Phe Leu Leu Ser Pro
173      370                 375                 380
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RAW SEQUENCE LISTING   DATE: 09/05/2002
PATENT APPLICATION: US/09/469,200C   TIME: 08:43:24

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176 Phe Tyr Gly Val Leu His Leu Phe Val Leu Gln Pro Leu Lys Leu Tyr
177 385                 390             395                 400
180 Ser Leu Phe Thr Ile Arg Asn Ala Asp Trp Gly Thr Arg Lys Lys Leu
181                 405             410                 415
184 Leu
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189 <211> LENGTH: 22
190 <212> TYPE: DNA
191 <213> ORGANISM: Synthetic
193 <400> SEQUENCE: 3
194 gctgatgaga caggtattaa gc                                        22
197 <210> SEQ ID NO: 4
198 <211> LENGTH: 20
199 <212> TYPE: DNA
200 <213> ORGANISM: Synthetic
202 <400> SEQUENCE: 4
203 atcaaattct ctgacattgc                                           20
206 <210> SEQ ID NO: 5
207 <211> LENGTH: 20
208 <212> TYPE: DNA
209 <213> ORGANISM: Synthetic
211 <400> SEQUENCE: 5
212 gactcagata cttatatcta                                           20
215 <210> SEQ ID NO: 6
216 <211> LENGTH: 17
217 <212> TYPE: DNA
218 <213> ORGANISM: Synthetic
220 <400> SEQUENCE: 6
221 tttttacgtg ttcccca                                              17
224 <210> SEQ ID NO: 7
225 <211> LENGTH: 1740
226 <212> TYPE: DNA
227 <213> ORGANISM: Paramecium bursaria chlorella virus
229 <400> SEQUENCE: 7
230 aagacttctt gaaagttaca atgggtaaaa atataatcat aatggtttcg tggtacacca    60
232 tcataacttc aaatctaatc gcggttggag gagcctctct aatcttggct ccggcaatta   120
234 ctgggtatgt tctacattgg aatattgctc tctcgacaat ctggggagta tcagcttatg   180
236 gtattttcgt ttttgggttt ttccttgcac aagttttatt ttcagaactg aacaggaaac   240
238 gtcttcgcaa gtggatttct ctcagaccta agggttggaa tgatgttcgt ttggctgtga   300
240 tcattgctgg atatcgcgag gatccttata tgttccagaa gtgcctcgag tctgtacgtg   360
242 actctgatta tggcaacgtt gcccgtctga tttgtgtgat tgacggtgat gaggacgatg   420
244 atatgaggat ggctgccgtt tacaaggcga tctacaatga taatatcaag aagcccgagt   480
246 ttgttctgtg tgagtcagac gacaaggaag gtgaacgcat cgactctgat ttctctcgcg   540
248 acatttgtgt cctccagcct catcgtggaa aacgggagtg tctttatact gggtttcaac   600
250 ttgcaaagat ggaccccagt gtcaatgctg tcgttctgat tgacagcgat accgttctcg   660
252 agaaggatgc tattctggaa gttgtatacc cacttgcatg cgatcccgag atccaagccg   720
254 ttgcaggtga gtgtaagatt tggaacacag acactctttt gagtcttctc gtcgcttggc   780
256 ggtactattc tgcgttttgt gtggagagga gtgcccagtc tttttcagg actgttcagt   840
258 gcgttggggg gccactgggt gcctacaaga ttgatatcat taaggagatt aaggacccct   900
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[handwritten annotation:] Invalid response - see error Summary sheet item 10

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260 ggatttccca gcgctttctt ggtcagaagt gtacttacgg tgacgaccgc cggctaacca      960
262 acgagatctt gatgcgtggt aaaaaggttg tgttcactcc atttgctgtt ggttggtctg     1020
264 acagtccgac caatgtgttt cggtacatcg ttcagcagac ccgctggagt aagtcgtggt     1080
266 gccgcgaaat ttggtacacc ctcttcgccg cgtggaagca cggtttgtct ggaatttggc     1140
268 tggcctttga atgtttgtat caaattacat acttcttcct cgtgatttac ctcttttctc     1200
270 gcctagccgt tgaggccgac cctcgcgccc agacagccac ggtgattgtg agcaccacgg     1260
272 ttgcattgat taagtgtggg tattttttcat tccgagccaa ggatattcgg gcgttttact     1320
274 ttgtgcttta tacatttgtt tacttttttct gtatgattcc ggccaggatt actgcaatga     1380
276 tgacgctttg ggacattggc tggggtactc gcggtggaaa cgagaagcct tccgttggca     1440
278 cccgggtcgc tctgtgggca aagcaatatc tcattgcata tatgtggtgg gccgcggttg     1500
280 ttggcgctgg agtttacagc atcgtccata actggatgtt cgattggaat tctctttctt     1560
282 atcgttttgc tttggttggt atttgttctt acattgtttt tattgttatt gtgctggtgg     1620
284 tttatttcac cggcaaaatt acgacttgga atttcacgaa gcttcagaag gagctaatcg     1680
286 aggatcgcgt tctgtacgat gcaactacca atgctcagtc tgtgtgattt ttcctgcaag     1740
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290 <211> LENGTH: 2937
291 <212> TYPE: DNA
292 <213> ORGANISM: Pastuerella Multocida
294 <400> SEQUENCE: 8
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299 gttgaatttc aaattaccaa atgcaaagaa aaactctcag cacatccttc tgttaattca      180
301 gcacatcttt ctgtaaataa agaagaaaaa gtcaatgttt gcgatagtcc gttagatatt      240
303 gcaacacaac tgttactttc caacgtaaaa aaattagtac tttctgactc ggaaaaaaac      300
305 acgttaaaaa ataaatggaa attgctcact gagaagaaat ctgaaaatgc ggaggtaaga      360
307 gcggtcgccc ttgtaccaaa agattttccc aaagatctgg ttttagcgcc tttacctgat      420
309 catgttaatg attttacatg gtacaaaaag cgaaagaaaa gacttggcat aaaacctgaa      480
311 catcaacatg ttggtctttc tattatcgtt acaacattca atcgaccagc aatttttatcg      540
313 attacattag cctgtttagt aaaccaaaaa acacattacc cgtttgaagt tatcgtgaca      600
315 gatgatggta gtcaggaaga tctatcaccg atcattcgcc aatatgaaaa taaattggat      660
317 attcgctacg tcagacaaaa agataacggt tttcaagcca gtgccgctcg gaatatggga      720
319 ttacgcttag caaaatatga ctttattggc ttactcgact gtgatatggc gccaaatcca      780
321 ttatgggttc attcttatgt tgcagagcta ttagaagatg atgatttaac aatcattggt      840
323 ccaagaaaat acatcgatac acaacatatt gacccaaaag acttcttaaa taacgcgagt      900
325 ttgcttgaat cattaccaga agtgaaaacc aataatagtg ttgccgcaaa aggggaagga      960
327 acagtttctc tggattggcg cttagaacaa ttcgaaaaaa cagaaaatct ccgcttatcc     1020
329 gattcgcctt tccgtttttt tgcggcgggt aatgttgctt tcgctaaaaa atggctaaat     1080
331 aaatccggtt tctttgatga ggaatttaat cactggggtg gagaagatgt ggaatttgga     1140
333 tatcgcttat tccgttacgg tagtttcttt aaaactattg atggcattat ggcctaccat     1200
335 caagagccac caggtaaaga aaatgaaacc gatcgtgaag cgggaaaaaa tattacgctc     1260
337 gatattatga gagaaaaggt cccttatatc tatagaaaac ttttaccaat agaagattcg     1320
339 catatcaata gagtacckttt agtttcaatt tatatcccag cttataactg tgcaaactat     1380
341 attcaacgtt gcgtagatag tgcactgaat cagactgttg ttgatctcga ggtttgtatt     1440
343 tgtaacgatg gttcaacaga taataccttta gaagtgatca ataagcttta tggtaataat     1500
345 cctagggtac gcatcatgtc taaaccaaat ggcggaatag cctcagcatc aaatgcagcc     1560
347 gtttcttttg ctaaaggtta ttacattggg cagttagatt cagatgatta tcttgagcct     1620
349 gatgcagttg aactgtgttt aaaagaattt ttaaaagata aaacgctagc ttgtgtttat     1680
351 accactaata gaaacgtcaa tccggatggt agcttaatcg ctaatggtta caattggcca     1740
353 gaattttcac gagaaaaact cacaacggct atgattgctc accactttag aatgttcacg     1800
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RAW SEQUENCE LISTING   DATE: 09/05/2002
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Input Set : A:\sequenc listing.txt
Output Set: N:\CRF4\09052002\I469200C.raw

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355 attagagctt ggcatttaac tgatggattc aatgaaaaaa ttgaaaatgc cgtagactat  1860
357 gacatgttcc tcaaactcag tgaagttgga aaatttaaac atcttaataa aatctgctat  1920
359 aaccgtgtat tacatggtga taacacatca attaagaaac ttggcattca aaagaaaaac  1980
361 cattttgttg tagtcaatca gtcattaaat agacaaggca taacttatta taattatgac  2040
363 gaatttgatg atttagatga aagtagaaag tatattttca ataaaaccgc tgaatatcaa  2100
365 gaagagattg atatcttaaa agatattaaa atcatccaga ataaagatgc caaaatcgca  2160
367 gtcagtattt tttatcccaa tacattaaac ggcttagtga aaaaactaaa caatattatt  2220
369 gaatataata aaaatatatt cgttattgtt ctacatgttg ataagaatca tcttacacca  2280
371 gatatcaaaa aagaaatact agccttctat cataaacatc aagtgaatat tttactaaat  2340
373 aatgatatct catattacac gagtaataga ttaataaaaa ctgaggcgca tttaagtaat  2400
375 attaataaat taagtcagtt aaatctaaat tgtgaataca tcatttttga taatcatgac  2460
377 agcctattcg ttaaaaatga cagctatgct tatatgaaaa aatatgatgt cggcatgaat  2520
379 ttctcagcat taacacatga ttggatcgag aaaatcaatg cgcatccacc atttaaaaag  2580
381 ctcattaaaa cttattttaa tgacaatgac ttaaaaagta tgaatgtgaa agggggcatca  2640
383 caaggtatgt ttatgacgta tgcgctagcg catgagcttc tgacgattat taaagaagtc  2700
385 atcacatctt gccagtcaat tgatagtgtg ccagaatata cactgaggga tatttggttc  2760
387 caatttgcac ttttaatctt agaaaagaaa accggccatg tatttaataa aacatcgacc  2820
389 ctgacttata tgccttggga acgaaaatta caatggacaa atgaacaaat tgaaagtgca  2880
391 aaaagaggag aaaatatacc tgttaacaag ttcattatta atagtataac tctataa     2937
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394 <210> SEQ ID NO: 9
395 <211> LENGTH: 972
396 <212> TYPE: PRT
397 <213> ORGANISM: Pastuerella Multocida

399 <400> SEQUENCE: 9
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402 1               5                   10                  15
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406             20                  25                  30
409 Lys Ile Val Glu Phe Gln Ile Thr Lys Cys Lys Glu Lys Leu Ser Ala
410         35                  40                  45
413 His Pro Ser Val Asn Ser Ala His Leu Ser Val Asn Lys Glu Glu Lys
414     50                  55                  60
417 Val Asn Val Cys Asp Ser Pro Leu Asp Ile Ala Thr Gln Leu Leu Leu
418 65                  70                  75                  80
421 Ser Asn Val Lys Lys Leu Val Leu Ser Asp Ser Glu Lys Asn Thr Leu
422             85                  90                  95
425 Lys Asn Lys Trp Lys Leu Leu Thr Glu Lys Lys Ser Glu Asn Ala Glu
426             100                 105                 110
429 Val Arg Ala Val Ala Leu Val Pro Lys Asp Phe Pro Lys Asp Leu Val
430         115                 120                 125
433 Leu Ala Pro Leu Pro Asp His Val Asn Asp Phe Thr Trp Tyr Lys Lys
434     130                 135                 140
437 Arg Lys Lys Arg Leu Gly Ile Lys Pro Glu His Gln His Val Gly Leu
438 145                 150                 155                 160
441 Ser Ile Ile Val Thr Thr Phe Asn Arg Pro Ala Ile Leu Ser Ile Thr
442             165                 170                 175
445 Leu Ala Cys Leu Val Asn Gln Lys Thr His Tyr Pro Phe Glu Val Ile
446             180                 185                 190
449 Val Thr Asp Asp Gly Ser Gln Glu Asp Leu Ser Pro Ile Ile Arg Gln
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VERIFICATION SUMMARY
                                        DATE: 09/05/2002
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